

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 08/15/2001

TIME: 08:22:46

Input Set : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

ENT 000

1.5

3 <110> APPLICANT: Johansen, Teit E.
 4 Wen-Yee Saw, Dinah
 6 <120> TITLE OF INVENTION: Novel Neurotrophic Factors
 8 <130> FILE REFERENCE: Novel Neurotrophic Factors
 10 <140> CURRENT APPLICATION NUMBER: US/09/804,615
 11 <141> CURRENT FILING DATE: 2001-03-12
 12 <150> PFIOP APPLICATION NUMBER: DANISH 1998 00904
 14 <151> PFIOP FILING DATE: 1998-07-06
 16 <150> PFIOP APPLICATION NUMBER: USSN 60/092,229
 17 <151> PFIOP FILING DATE: 1998-07-09
 19 <150> PFIOP APPLICATION NUMBER: DANISH 1998 01048
 20 <151> PFIOP FILING DATE: 1998-08-19
 21 <150> PFIOP APPLICATION NUMBER: USSN 60/097,774
 23 <151> PFIOP FILING DATE: 1998-08-25
 25 <150> PFIOP APPLICATION NUMBER: USSN 60/103,908
 26 <151> PFIOP FILING DATE: 1998-10-13
 28 <150> PFIOP APPLICATION NUMBER: DANISH 1998 01265
 29 <151> PFIOP FILING DATE: 1998-10-06
 31 <150> PFIOP APPLICATION NUMBER: U.S.S.N 09/347,613
 32 <151> PFIOP FILING DATE: 1999-07-02
 34 <160> NUMBER OF SEQ ID NOS: 40
 36 <170> SOFTWARE: PatentIn Ver. 2.1
 38 <180> SEQ ID NO: 1
 39 <110> LENGTH: 865
 40 <210> TYPE: DNA
 41 <213> ORGANISM: Homo sapiens
 43 <210> FEATURE:
 44 <211> NAME/KEY: CDS
 45 <212> LOCATION: (120)..(719)
 47 <210> FEATURE:
 48 <211> NAME/KEY: 5'UTR
 49 <212> LOCATION: (1)..(119)
 51 <210> FEATURE:
 52 <211> NAME/KEY: 3'UTR
 53 <212> LOCATION: (121)..(865)
 55 <210> FEATURE:
 56 <211> NAME/KEY: sig_peptide
 57 <212> LOCATION: (120)..(170)
 59 <210> FEATURE:
 60 <211> NAME/KEY: mat_peptide
 61 <212> LOCATION: (175)..(719)
 63 <210> FEATURE:
 64 <211> NAME/KEY: misc_structure
 65 <212> LOCATION: (61)..(66)
 66 <223> OTHER INFORMATION: CARBOHYD: Glycylated Asparagine at Asn57
 67 <220> FEATURE:
 68 <221> NAME/KEY: misc_structure

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 08/15/2001

TIME: 16:22:46

Input Set : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

```

70 <222> LOCATION: (426)..(623)
71 <223> OTHER INFORMATION: DISULFID - Cys4-Cys73 disulfide bridge
72 <224> FEATURE:
73 <221> NAME/KEY: misc_structure
74 <222> LOCATION: (137)..(707)
75 <223> OTHER INFORMATION: DISULFID: Cys4-Cys101 disulfide bridge
76 <224> FEATURE:
77 <221> NAME/KEY: misc_structure
78 <222> LOCATION: (519)..(713)
79 <223> OTHER INFORMATION: DISULFID: Cys19-Cys103 disulfide bridge
80 <224> FEATURE:
81 <221> NAME/KEY: misc_structure
82 <222> LOCATION: (616)..(619)
83 <223> OTHER INFORMATION: DISULFID: Cys72-Cys72 interchain disulfide bridge
84 <400> SEQUENCE: 1
85 ctaggagagcc atgcccggcc tgatctcagc ccgaggacag cccctccttg aggtccctcc 60
86 tccccagcc caccctgggtg cctctttct ccttgaggtt ccaattgggtc tctccgggc 119
87 atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167
88 Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
89 -45 -90 -85 -80
90 gtc gca gag gcc tcc ctg gcc tcc ggc ccc cgc agc cct gcc acc agc 215
91 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
92 -75 -1 -65
101 aca gcc ccc ccg cct gtc ctg gag tcc acc ggc agc cac ctg ccg ggc 263
102 Glu Gly Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
103 -60 -55 -50
105 gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg ccg cgc cgc 311
106 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Pro Arg Arg
107 -45 -40 -35
109 aca cac ttc tgg gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct 359
110 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
111 -30 -25 -20
113 tcc ccg cgg gtc cgc gcc gcc cgg ctg cgg gcc cgg gca gcc cgc tgc 407
114 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
115 -15 -10 -5 -1 1
117 agc agc ggg ggc ggc ggc tcc cgc ctg agc tgc cag ctg ctg ccg gtc 455
118 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Glu Leu Val Pro Val
119 5 10 15
121 agc gcc ctg gcc ctg gtc ccc agc tcc acc agc ctg gtc cgt ttc arg 503
122 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Ala Leu Val Arg Phe Arg
123 20 25 30
125 ttc tgc acc gcc tcc ttc acc gcc ttc ttc ttc ttc ttc ttc ttc ttc 551
126 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Phe His Asp Leu Ser
127 35 40 45
129 ctg gcc acc gca ctg gcc gcc ttc ttc ttc ttc ttc ttc ttc ttc ttc 600
130 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
131 50 55 60
133 ttc acc gtc acc acc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 647
134 Arg Pro Val Ser His Pro Cys Cys Arg His Thr Arg Tyr His Ala Val

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 09-10-2001

TIME: 11:22:40

Input File : A:\Bgn-111.app

Output File: N:\CRF3\08132001\I804615.raw

```

135          70          75          80
137 tcc ttc atg gag gtc aac agc acc ttc att att atg gac agc atc ttc      895
138 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
139          85          90          95
141 ggc acc ggc ttc ggc tgc ctg ggc tga ggg ttc atc ccc agc agc ttc ttc      940
142 Ala Thr Ala Cys Gly Cys Leu Gly
143          100          105
144 gacccttacc ggtggtctctt cctgcttggc atttcttctt atagttcttacc tttttttt      985
145 ctctagccag ggaagaagga ctcaaatgt gaaatctt ggggttggt gattga      *65
11 <210> SEQ ID NO: 2
131 <211> LENGTH: 200
132 <212> TYPE: PRT
133 <213> ORGANISM: Homo sapiens
134 <400> SEQUENCE: 2
136 Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
137 -95          -90          -85          -80
138 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
139          -75          -70          -65
140 Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
141          -60          -55          -50
142 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Ala Arg
143          -45          -40          -35
144 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
145 -30          -25          -20
146 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
147 -15          -10          -5          -1    1
148 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
149          5          10          15
150 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
151          20          25          30
152 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
153          35          40          45
154 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
155          50          55          60          65
156 Arg Pro Val Ser Gln Pro Cys Cys Arg Arg Thr Arg Tyr Glu Ala Val
157          70          75          80
158 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
159          85          90          95
160 Ala Thr Ala Cys Gly Cys Leu Gly
161          100          105
167 <210> SEQ ID NO: 3
168 <211> LENGTH: 861
169 <212> TYPE: CNA
170 <213> ORGANISM: Homo sapiens
171 <220> FEATURE:
172 <221> NAME KEY: CNA
173 <222> LOCATION: 1..100
174 <223> FEATURE:
175 <224> NAME KEY: CNA

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 8-15-01

TIME: 11:02:40

Input Set : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

```

208 <220> LOCATION: (1)..(6)
210 <220> FEATURE:
211 <220> NAME KEY: CINTR
212 <220> LOCATION: (16)..(66)
214 <220> FEATURE:
215 <220> NAME KEY: sig_peptide
216 <220> LOCATION: (7)..(174)
218 <220> FEATURE:
219 <220> NAME KEY: mat_peptide
221 <220> LOCATION: (298)..(717)
223 <220> FEATURE:
224 <220> NAME KEY: mat_peptide
225 <220> LOCATION: (370)..(717)
227 <220> FEATURE:
228 <220> NAME KEY: mat_peptide
229 <220> LOCATION: (379)..(717)
231 <220> FEATURE:
232 <220> NAME KEY: misc_structure
233 <220> LOCATION: (661)..(663)
235 <220> OTHER INFORMATION: CARBOHYD: glycosylated Asparagine as Asn122
237 <220> FEATURE:
238 <220> NAME KEY: misc_structure
239 <220> LOCATION: (424)..(621)
241 <220> OTHER INFORMATION: DISULFID: Cys43-Cys108 disulfide bridge
243 <220> FEATURE:
244 <220> NAME KEY: misc_structure
245 <220> LOCATION: (505)..(705)
247 <220> OTHER INFORMATION: DISULFID: Cys70-Cys136 disulfide bridge
249 <220> FEATURE:
250 <220> NAME KEY: misc_structure
251 <220> LOCATION: (517)..(711)
253 <220> OTHER INFORMATION: DISULFID: Cys74-Cys138 disulfide bridge
255 <220> FEATURE:
256 <220> NAME KEY: misc_structure
257 <220> LOCATION: (616)..(616)
259 <220> OTHER INFORMATION: DISULFID: Cys107-Cys137 interchain disulfide
261 bridge
263 <400> SEQUENCE: 3
264 gaaacc atg cca gga cta atc tca gcc cca cca cca cca cca cca cca 47
265 Met Pro Gly Leu Ile Ser Ala Arg Gly Ala Pro Leu Leu Ala
266 -35 -2 -1
267 gtc ctt cct cca caa gcc cca cca cca cca cca cca cca cca cca 48
268 Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Pro Leu Pro Ala
269 -35 -2 -1
270 cca ctt gtt cca cca cca cca cca cca cca cca cca cca cca cca 144
271 Pro Leu Gly Leu Gln Ala Gln Ile Ala Leu Thr Ile Thr Leu Ala Ala
272 -35 -2 -1
273 atg gtt cca cca cca cca cca cca cca cca cca cca cca cca cca 145
274 Leu Ala Leu Leu Ser Gln Val Ala His Ala Ser Leu Gly Ser Ala Pro

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 08/15/2001

TIME: 14:31:46

Input File : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

```

271      -50      -45      -4
273 ggc agc act gac ccc ggc gac ggc ccc ccc act ccc ccc ccc ccc ccc 340
274 Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Leu Val Leu Ala Ser Pro
275 -35      -30      -25
277 gcc ggc gac ctg ccc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 345
278 Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg
279 -20      -15
281 gcc cgg cgg cgg cgg cgg cgg cgg cgg cgg cgg cgg cgg cgg cgg 350
282 Ala Arg Arg Pro Pro Pro Glu Pro Ser Arg Pro Ala Pro Pro Pro
283 -10      -5
285 gca ccc ccc ccc ccc ccc ccc ccc ccc ccc ccc ccc ccc ccc ccc 355
286 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
287 15      20      25
289 ggc cgg ggc aac cgc gct cgg gca ggc ggc ggc ggc ggc ggc ggc 360
290 Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
291 30      35      40      45
293 cgc tgc cag ctg gtg cgg gtg cgc ggc ctc ggc ctg ggc cag cgc tcc 365
294 Arg Ser Glu Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
295 50      55      60
297 gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc ggc 370
298 Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Ala
299 65      70      75
301 cgc tcc cca cag gac ctc agc ctg gcc agc cta ctg ggc gcc ggc gcc 375
302 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
303 80      85      90
305 ctg cga cgg ccc cgg ggc tcc cgg ccc gtc agc aac ccc tgc tcc cga 380
306 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Glu Pro Cys Cys Arg
307 95      100      105
309 ccc acg cgc tac gaa gag gtc tcc ttc atg gac gtc aac agc acc tgg 385
310 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
311 110      115      120      125
313 aca acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc 390
314 Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
315 130      135      140
317 ttgagggtctg ctccagggt ttgcagactg gacccctacc ggtggtcttt cctccctggg 395
318 aacctccgc agatccac tagccaggg cctccagcag ggcagaaag ccccaactc 400
319 agagggcctt gccctgggt gatg 405
320 <210> SEQ ID NO: 4
321 <211> LENGTH: 137
322 <212> TYPE: PRT
323 <213> ORGANISM: Homo sapiens
324 <400> SEQUENCE: 4
325 Met Pro Gly Leu Ile Ser Ala Arg Gly Glu Pro Leu Leu Ala Val Leu
326 -90      -85      -80
328 Pro Pro His Ala His Leu Gly Ala Leu Ile Leu Pro His Ala Pro Leu
329 -75      -70      -65
331 Gly Leu Ser Ala His Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala
332 -60      -55      -50
334 Leu Leu Ser Ser Val Ala His Ala Ser Leu Gly Ser Ala Pro Arg Ser

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/804,615

DATE: 11/14/2001

TIME: 11:11:47

Input Set : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

L:10 M:258 C: Current Application Number differs, Replaced Current Application Number
 L:411 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1
 L:411 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1
 L:411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:443 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1
 L:443 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1
 L:443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:478 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1
 L:478 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1
 L:478 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:1091 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:27
 L:1091 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:27
 L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27